

Blast 2 Sequences

Exhibit 3

NCBI	Entrez	BLAST 2 sequences	BLAST	Example	Help
------	--------	-------------------	-------	---------	------

BLAST 2 SEQUENCES

This tool produces the alignment of two given sequences using BLAST engine for local alignment. The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site.
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch: ☐ Use Mega BLAST Strand option Open gap: and extension gap: penalties
gap x_dropoff: expect: word size: Filter ☒Sequence 1 Enter accession or GI or download from file Browse...
or sequence in FASTA format from: to: Sequence 2 Enter accession or GI or download from file Browse...
or sequence in FASTA format from: to:

cgaccaagtctagagcgcttccggt

Comments and suggestions to: blast-help@ncbi.nlm.nih.gov
Credits to: [Tatiana Tatusov](#) and [Tom Madden](#)

**Blast 2 Sequences results**

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.2 [Dec-14-2001]Match: Mismatch: gap open: gap extension: x_dropoff: expect: wordsize: ☐ Filter

Sequence gi Homo sapiens endothelial differentiation, sphingolipid G-protein- Length 2753
1 13017635 coupled receptor, 1 (EDG1), mRNA

Sequence icl|s:q_2 Length 25
2

No significant similarity was found